WHAT IS CLAIMED IS:

Sub a1

1. A method of detecting mutation in the base sequence of nucleic acid, including:

(A) a bonding step of hybridizing an object of analysis consisting of nucleic acid or a nucleic acid fragment including a plurality of inspected sites to be subjected to inspection of mutation in the base sequence with a plurality of types of oligonucleotides having base sequence complementary to any of the inspected sites having normal base sequence and labeled to be discriminable from each other for forming duplexes; and

(B) a detection step of employing an ion pair chromatograph comprising a reversed phase column serving as a separation column and a detector capable of discriminating and detecting the labeled oligonucleotides and setting the separation column at a temperature causing difference in stability between hetero- and homoduplexes included in the duplexes for analyzing the object of analysis.

2. The mutation detecting method according to claim 1, wherein

the oligonucleotides are labeled with the fluorescent materials.

Sub C1

3. The mutation detecting method according to claim 1, wherein

the separation column is set at the melting temperature of the heteroduplex.

Sub a2

4. The mutation detecting method according to claim 1,

observing a chromatogram of labels obtained through the detection step (B) for determining an inspected site corresponding to a label having a single peak as non-mutational while determining an inspected site corresponding to a label having two peaks as mutational.

SUB C1 CONT.

5. The mutation detecting method according to claim 1, including an amplification step of amplifying the object of analysis in advance of the bonding step (A).

6. The mutation detecting method according to claim 5, wherein

the amplification step is a single PCR step.